

# SEQUENCE LISTING

<110> Pecker, Iris  
 Vlodavsky, Israel  
 Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY  
 AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

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<170> PatentIn version 3.5

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 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
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 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
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 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
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 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser  
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 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
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 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu  
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 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr  
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 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile  
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 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly  
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 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala  
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 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro  
 385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr  
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Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg  
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Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
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Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
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Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
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Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg  
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Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu  
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Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala  
50 55 60  
aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag 299  
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Gly Ser Pro Lys  
65 70 75  
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Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu	
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Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys	
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Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys	115	120	125
Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp	130	135	140
Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe	145	150	155
Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe	165	170	175
Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu	180	185	190
Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu	195	200	205
Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn	210	215	220
Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser	225	230	235
Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser	245	250	255
Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg	260	265	270
Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu	275	280	285
Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr	290	295	300
Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile	305	310	315
Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly	325	330	335
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 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg  
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 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
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Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg  
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Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu  
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Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala  
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Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys  
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Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr  
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16



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gatcttggat	tctggccacc tccgcaccct ttggatgggt gtggatgatt tcaaaagtgg 360

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Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser  
 65 70 75 80

Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe  
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Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser  
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Gln Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val  
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Arg Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser  
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Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn  
 180 185 190

Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr  
 195 200 205

Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys  
 210 215 220

Ala His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu  
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 Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser Pro  
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 Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser Gln  
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 Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val Leu  
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 Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu Arg  
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Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile	165	170	175	
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Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser	180	185	190	
tcc aac gcc cag ctt ctc ctt gac tac tgc tct tcc aag ggt tat aac				1220
Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn	195	200	205	
atc tcc tgg gaa ctg ggc aat gag ccc aac agt ttc tgg aag aaa gct				1268
Ile Ser Trp Glu Leu Leu Asn Glu Pro Asn Ser Phe Trp Lys Lys Ala	210	215	220	225
cac att ctc atc gat ggg ttg cag tta gga gaa gac ttt gtg gag ttg				1316
His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu Leu	230	235	240	
cat aaa ctt cta caa agg tca gct ttc caa aat gca aaa ctc tat ggt				1364
His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr Gly	245	250	255	
cct gac atc ggt cag cct cga ggg aag aca gtt aaa ctg ctg agg agt				1412
Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg Ser	260	265	270	
ttc ctg aag gct ggc gga gaa gtg atc gac tct ctt aca tgg cat cac				1460
Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu Thr Trp His His	275	280	285	
tat tac ttg aat gga cgc atc gct acc aaa gaa gat ttt ctg agc tct				1508
Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser Ser	290	295	300	305
gat gcg ctg gac act ttt att ctc tct gtg caa aaa att ctg aag gtc				1556
Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys Val	310	315	320	
act aaa gag atc aca cct ggc aag aag gtc tgg ttg gga gag acg agc				1604
Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser	325	330	335	
tca gct tac ggt ggc ggt gca ccc ttg ctg tcc aac acc ttt gca gct				1652
Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asn Thr Phe Ala Ala	340	345	350	
ggc ttt atg tgg ctg gat aaa ttg ggc ctg tca gcc cag atg ggc ata				1700
Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Gln Met Gly Ile	355	360	365	
gaa gtc gtg atg agg cag gtg ttc ttc gga gca ggc aac tac cac tta				1748
Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu	370	375	380	385
gtg gat gaa aac ttt gag cct tta cct gat tac tgg ctc tct ctt ctg				1796
Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu	390	395	400	
ttc aag aaa ctg gta ggt ccc agg gtg tta ctg tca aga gtg aaa ggc				1844
Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly	405	410	415	
cca gac agg agc aaa ctc cga gtg tat ctc cac tgc act aac gtc tat				1892
Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr	420	425	430	
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 His Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg Lys  
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 Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu Leu  
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 Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser Ala  
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 515 520 525  
 aaa atc gct gct tgt ata tgaaaataaa aggcatacgg taccctgag 2228  
 Lys Ile Ala Ala Cys Ile  
 530 535  
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 35 40 45  
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 50 55 60  
 Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser  
 65 70 75 80  
 Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe  
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 Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser  
 100 105 110  
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 115 120 125

Leu Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu  
 130 135 140  
 Arg Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser  
 145 150 155 160  
 Ser Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu  
 165 170 175  
 Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn  
 180 185 190  
 Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr  
 195 200 205  
 Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys  
 210 215 220  
 Ala His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu  
 225 230 235 240  
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 245 250 255  
 Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg  
 260 265 270  
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 275 280 285  
 His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser  
 290 295 300  
 Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys  
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 Val Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr  
 325 330 335  
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 340 345 350  
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 355 360 365  
 Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His  
 370 375 380  
 Leu Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu  
 385 390 395 400  
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                          485                      490                      495  
 Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser  
                          500                      505                      510  
 Ala Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val Ile Arg Asn  
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 gcgtacttga gatttggcgg caccaagact gacttcctta tttttgatcc caacaacgaa 300  
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Tyr Thr Lys Arg Leu Phe Gln Ser Val Ser Pro Ser Phe Leu Ser Ile  
35 40 45

Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu Thr Phe Leu  
50 55 60

Ser Ser Pro Arg Leu Arg Ala Leu Ser Arg Gly Leu Ser Pro Ala Tyr  
65 70 75 80

Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Asn  
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Leu Lys Met Val Asp Glu Gln Thr Xaa Pro Ala Leu Thr Glu Lys Pro

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				Ser	Val	Pro
					25	Ala
						Phe
						Ser
						Tyr
						30
						Gly
						Phe
Phe	Val	Ile	Arg	Asn	Ala	Lys
		35				
						Ile
						40
						Ala
						Ala
						Cys
						Ile